

SEQUENCE LISTING

INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 994 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 41..508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGAGAGGGG GAGAACAGAC AACGGGCGGC GGGGAGCAGC	ATG GAT CCG GCG GCG	55
	Met Asp Pro Ala Ala	
	1 5	
GGG AGC AGC ATG GAG CCT TCG GCT GAC TGG GTG GCC ACG GCC GCG GCC		103
Gly Ser Ser Met Glu Pro Ser Ala Asp Trp	Leu Ala Thr Ala Ala Ala	
	10 15 20	
CGG GGT CGG GTA GAG GAG GTG CGG GCG GTG CTG GAG GCG GTG GCG CTG		151
Arg Gly Arg Val Glu Glu Val Arg Ala	Leu Leu Glu Ala Val Ala Leu	
	25 30 35	
CCC AAC GCA CCG AAT AGT TAC GGT CGG AGG CCG ATC CAG GTC ATG ATG		199
Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro Ile Gln Val Met Met		
	40 45 50	
ATG GGC AGC GCC CGA GTG GCG GAG CTG CTG CTG CTC CAC GGC GCG GAG		247
Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu His Gly Ala Glu		
	55 60 65	
CCC AAC TGC GCC GAC CCC GGC ACT CTC ACC CGA CCC GTG CAC GAC GCT		295
Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val His Asp Ala		
	70 75 80 85	
GCC CGG GAG GGC TTC CTG GAC ACG CTG GTG GTG CTG CAC CGG GCC GGG		343
Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly		
	90 95 100	
GCG CGG CTG GAC GTG CGC GAT GCC TGG GGC CGT CTG CCC GTG GAC CTG		391
Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu		
	105 110 115	
GCT GAG GAG CTG GGC CAT CGC GAT GTC GCA CGG TAC CTG GCG GCG GCT		439
Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg Ala Ala		
	120 125 130	
GCG GGG GGC ACC AGA GGC AGT AAC CAT GCC CGC ATA GAT GCC GCG GAA		487

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Sub. I

Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg Ile Asp Ala Ala Glu
135 140 145

GGT CCC TCA GAC ATC CCC GAT TGAAAGAACC AGAGAGGCTC TGAGAAACCT 538
Gly Pro Ser Asp Ile Pro Asp
150 155

CGGGAAACTT AGATCATCAG TCACCGAAGG TCCTACAGGG CCACAACGTC CCACGCCACA 598
ACCCACCCCG CTTTCGTAGT TTTCATTAG AAAATAGAGC TTTTAAAAAT GTCTGCGCTT 658
TTAACGTAGA TATAAGCCTT CCCCCTACTAC CGTAAATGTC CATTATATATC ATTTTTTATA 718
TATTCTTATA AAAATGTAAA AAAGAAAAAC ACCGCTTCTG CCTTTTCACT GTGTTGGAGT 778
TTTCTGGAGT GAGCACTCAC GCCCTAAGCG CACATTCATG TGGGCATTTC TTGCGAGCCT 838
CGCAGCCTCC GGAAGCTGTC GACTTCATGA CAAGCATTTT GTGAAGTAGG GAAGCTCAGG 898
GGGGTTACTG GCTTCTCTTG AGTCACACTG CTAGCAAATG GCAGAACCAG AGCTCAAATA 958
AAAATAAAAT TATTTTCATT CATTACTCA AAAAAA 994

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 156 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Pro Ala Ala Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu
1 5 10 15

Ala Thr Ala Ala Ala Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu
20 25 30

Glu Ala Val Ala Leu Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro
35 40 45

Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu
50 55 60

Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg
65 70 75 80

Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val
85 90 95

Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg
100 105 110

Leu Pro Val Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg
115 120 125

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Tyr Leu Arg Ala Ala Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg
 130 135 140
 Ile Asp Ala Ala Glu Gly Pro Ser Asp Ile Pro Asp
 145 150 155

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 837 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 328..738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAGGACTCCG CGACGGTCCG CACCCCTGCGG CCAGAGCGGG TTTGAGCTCG GCTGCTTCCG 60
 CGCTAGGCGC TTTTTCCTCAG AAGCAATCCA GGCGCGCCCG CTGGTTCTTG AGCGCCAGGA 120
 AAAGCCCGGA GCTAACGACC GGCCGCTCCG CACTGCACGG GGCCCCAAGC CGCAGAAGAA 180
 GGACGACGGG AGGGTAATGA AGCTGAGCCC AGGTCTCCTA GGAAGGAGAG AGTGCGCCGG 240
 AGCAGCGTGG GAAAGAAGGG AAGAGTGTCTG TTAAGTTTAC GGCCAACGGT GGATTATCCG 300
 GGCCGCTGCG CGTCTGGGGG CTGCGGGA ATG CGC GAG GAG AAC AAG GGC ATG 351
 Met Arg Glu Glu Asn Lys Gly Met
 1 5
 CCC AGT GGG GGC GGC AGC GAT GAG GGT CTG GCC ACG CCG GCG CGG GGA 399
 Pro Ser Gly Gly Gly Ser Asp Glu Gly Leu Ala Thr Pro Ala Arg Gly
 10 15 20
 CTA GTG GAG AAG GTG CGA CAC TCC TGG GAA GCC GGC GCG GAT CCC AAC 447
 Leu Val Glu Lys Val Arg His Ser Trp Glu Ala Gly Ala Asp Pro Asn
 25 30 35 40
 GGA GTC AAC CGT TTC GGG AGG CGC GCG ATC CAG GTC ATG ATG ATG GGC 495
 Gly Val Asn Arg Phe Gly Arg Arg Ala Ile Gln Val Met Met Met Gly
 45 50 55
 AGC GGC CGC GTG GCG GAG CTG CTG CTG CTC CAC GGC GCG GAG CCC AAC 543
 Ser Ala Arg Val Ala Glu Leu Leu Leu His Gly Ala Glu Pro Asn
 60 65 70
 TGC GCA GAC CCT GCC ACT CTC ACC CGA CCG GTG CAT GAT GCT GCC CGG 591
 Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val His Asp Ala Ala Arg

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75	80	85	
GAG GGC TTC CTG GAC ACG CTG GTG GTG CTG CAC CGG GCC GGG GCG CGG			639
Glu Gly Phe Leu Asp Thr	Leu Val Val Leu His Arg Ala Gly Ala Arg		
90	95	100	
CTG GAC GTG CGC GAT GCC TGG GGT CGT CTG CCC GTG GAC TTG GCC GAG			687
Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu Ala Glu			
105	110	115	120
GAG CGG GGC CAC CGC GAC GTT GCA GGG TAC CTG CGC ACA GCC ACG GGG			735
Glu Arg Gly His Arg Asp Val Ala Gly Tyr Leu Arg Thr Ala Thr Gly			
125	130	135	
GAC TGACGCCAGG TTCCCCAGCC GCCCACACG ACTTTATTTT ATTACCCAAT			788
Asp			
TTCCCCACCCC CACCCACCTA ATTCGATGAA GGCTGCCAAG GGGGAGCGG			837

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 137 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Glu Glu Asn Lys Gly Met Pro Ser Gly Gly Gly Ser Asp Glu			
1	5	10	15
Gly Leu Ala Thr Pro Ala Arg Gly Leu Val Glu Lys Val Arg His Ser			
20	25	30	
Trp Glu Ala Gly Ala Asp Pro Asn Gly Val Asn Arg Phe Gly Arg Arg			
35	40	45	
Ala Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu			
50	55	60	
Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr			
65	70	75	80
Arg Pro Val His Asp Ala Ala Arg Gly Phe Leu Asp Thr Leu Val			
85	90	95	
Val Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly			
100	105	110	
Arg Leu Pro Val Asp Leu Ala Glu Glu Arg Gly His Arg Asp Val Ala			
115	120	125	
Gly Tyr Leu Arg Thr Ala Thr Gly Asp			

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135

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 853 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 213..587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGAGTACAGC AGCGGGAGCA TGGGTCGCAG GTTCTTGGTC ACTGTAAGGA TTCAGCGCGC	60
GGGCCGCCCA CTCCAAGAGA GGGTTTTCTT GGTGAAGPTC GTGCGATSCC GGAGACCCAG	120
GACAGCGAGC TGCCTCTGG CTTCGTGAA CATCTTGTG AGGCTAGAGA GGATCTTGAG	180
AAGAGGGCCG CACCGGAATC CTGGACCAGG TG ATG ATG ATG GGC AAC GTT CAC	233
Met Met Met Gly Asn Val His	
1 5	
GTA GCA GCT CTT CTG CTC AAC TAC GGT GCA GAT TCG AAC TGC GAG GAC	281
Val Ala Ala Leu Leu Asn Tyr Gly Ala Asp Ser Asn Cys Glu Asp	
10 15 20	
CCC ACT ACC TTC TCC CGC CCG GTG CAC GAC GCA GCG CGG GAA GGC TTC	329
Pro Thr Thr Phe Ser Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe	
25 30 35	
CTG GAC ACG CTG GTG GTG CTG CAC GGG TCA GGG GCT CGG CTG GAT GTG	377
Leu Asp Thr Leu Val Val Leu His Gly Ser Gly Ala Arg Leu Asp Val	
40 45 50 55	
CGC GAT GCC TGG GGT CGC CTG CCG CTC GAC TTG GCC CAA GAG CGG GGA	425
Arg Asp Ala Trp Gly Arg Leu Pro Leu Asp Leu Ala Gln Glu Arg Gly	
60 65 70	
CAT CAA GAC ATC GTG CGA TAT TTG CGT TCC GCT GGG TGC TCT TTG TGT	473
His Gln Asp Ile Val Arg Tyr Leu Arg Ser Ala Gly Cys Ser Leu Cys	
75 80 85	
TCC GCT GGG TGG TCT TTG TGT ACC GCT GGG AAC GTC GCC CAG ACC GAC	521
Ser Ala Gly Trp Ser Leu Cys Thr Ala Gly Asn Val Ala Gln Thr Asp	
90 95 100	
GGG CAT AGC TTC AGC TCA AGC ACG CCC AGG GCC CTG GAA CTT GGC GGC	569
Gly His Ser Phe Ser Ser Ser Thr Pro Arg Ala Leu Glu Leu Arg Gly	
105 110 115	

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CAA TCC CAA GAG CAG AGC TAAATCCGCC TCAGCCCGCC TTTTCTTCT 617
Gln Ser Gln Glu Gln Ser
120 125

TAGCTTCACT TCTAGCGATG CTAGCGTGTC TAGCATGTGG CTTTAAAAAA TACATAATAA 677

TGCTTTTTTT GCAATCACGG GAGGGAGCAG AGGGAGGGAG CAGAAGGAGG GAGGAGGGA 737

GGGAGGGACC TGGACAGGAA AGGAATGGCA TGAGAAACTG AGCGAAGGCG CCCGCGAAGG 797

GAATAATGGC TGGATTGTTT AAAAAAATAA AATAAGATA CTTTTAAAAA TGTCAA 853

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Met Met Gly Asn Val His Val Ala Ala Leu Leu Leu Asn Tyr Gly
1 5 10 15
Ala Asp Ser Asn Cys Glu Asp Pro Thr Thr Phe Ser Arg Pro Val His
20 25 30
Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Gly
35 40 45
Ser Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Leu
50 55 60
Asp Leu Ala Gln Glu Arg Gly His Gln Asp Ile Val Arg Tyr Leu Arg
65 70 75 80
Ser Ala Gly Cys Ser Leu Cys Ser Ala Gly Trp Ser Leu Cys Thr Ala
85 90 95
Gly Asn Val Ala Gln Thr Asp Gly His Ser Phe Ser Ser Ser Thr Pro
100 105 110
Arg Ala Leu Glu Leu Arg Gly Gln Ser Gln Glu Gln Ser
115 120 125

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCA CTC CTG GAA GCC GGC GCA GAT CCC AAC GCC CTG AAC CGC TTC GGG	48
Ala Leu Leu Glu Ala Gly Ala Asp Pro Asn Ala Leu Asn Arg Phe Gly	
1 5 10 15	
AGG CGC CCA ATC CAG GTC ATG ATG ATG GGC AGC GCC AGG GTG GCA GAG	96
Arg Arg Pro Ile Gln Val Met Met Gly Ser Ala Arg Val Ala Glu	
20 25 30	
CTG CTG CTG CTC CAC GGA GCA GAA CCC AAC TGC GCC GAC CCT GCC ACC	144
Leu Leu Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr	
35 40 45	
CTT ACC AGA CCT GTG CAC GAC GCA GCT CGG GAA GGC TTC CTG GAC ACG	192
Leu Thr Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr	
50 55 60	
CTT GTC GTG CTG CAC CGG GCA GGG CGG CGG TTG GAT GTG	231
Leu Val Val Leu His Arg Ala Gly Ala Arg Leu Asp Val	
65 70 75	

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala Leu Leu Glu Ala Gly Ala Asp Pro Asn Ala Leu Asn Arg Phe Gly	
1 5 10 15	
Arg Arg Pro Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu	
20 25 30	
Leu Leu Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr	
35 40 45	
Leu Thr Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr	
50 55 60	
Leu Val Val Leu His Arg Ala Gly Ala Arg Leu Asp Val	
65 70 75	

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(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Thr Ser Arg Tyr Glu Pro Val Ala Glu Ile Gly Val Gly Ala
1 5 10 15

Tyr Gly Thr Val Tyr Lys Ala Xaa Asp Pro His Ser Gly His Phe Val
20 25 30

Ala Leu Lys Ser Val Arg Val Pro Asn Gly Gly Gly Gly Gly Gly
35 40 45

Leu Pro Ile Ser Thr Val Arg Glu Val Ala Leu Leu Arg Arg Leu Glu
50 55 60

Ala Phe Glu His Pro Asn Val Val Arg Leu Met Asp Val Cys Ala Thr
65 70 75 80

Ser Arg Thr Asp Arg Glu Ile Lys Val Thr Leu Val Phe Glu His Val
85 90 95

Asp Gln Asp Leu Arg Thr Tyr Leu Asp Lys Ala Pro Pro Pro Gly Leu
100 105 110

Pro Ala Glu Thr Ile Lys Asp Leu Met Arg Gln Phe Leu Arg Gly Leu
115 120 125

Asp Phe Leu His Ala Asn Cys Ile Val His Arg Asp Leu Lys Pro Glu
130 135 140

Asn Ile Leu Val Thr Ser Gly Gly Thr Val Lys Leu Ala Asp Phe Gly
145 150 155 160

Leu Ala Arg Ile Tyr Ser Tyr Gln Met Ala Leu Thr Pro Val Val Val
165 170 175

Thr Leu Trp Tyr Arg Ala Pro Glu Val Leu Leu Gln Ser Thr Tyr Ala
180 185 190

Thr Pro Val Asp Met Trp Ser Val Gly Cys Ile Phe Ala Glu Met Phe
195 200 205

Arg Arg Lys Pro Leu Phe Cys Gly Asn Ser Glu Ala Asp Gln Leu Gly
210 215 220

Lys Ile Phe Asp Leu Ile Gly Leu Pro Pro Glu Asp Asp Trp Pro Arg

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225		230		235		240
Asp Val Ser Leu Pro Arg Gly Ala Phe Pro Pro Arg Gly Pro Arg Pro						
	245			250		255
Val Gln Ser Val Val Pro Glu Met Glu Glu Ser Gly Ala Gln Leu Leu						
	260			265		270
Leu Glu Met Leu Thr Phe Asn Pro His Lys Arg Ile Ser Ala Phe Arg						
	275		280		285	
Ala Leu Gln His Ser Tyr Leu His Lys Asp Glu Gly Asn Pro Glu						
	290		295		300	

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Glu Lys Asp Gly Leu Cys Arg Ala Asp Gln Gln Tyr Glu Cys Val							
1		5		10		15	
Ala Glu Ile Gly Glu Gly Ala Tyr Gly Lys Val Phe Lys Ala Xaa Asp							
	20		25		30		
Leu Lys Asn Gly Gly Arg Phe Val Ala Leu Lys Arg Val Arg Val Gln							
	35		40		45		
Thr Gly Glu Gln Gly Met Pro Leu Ser Thr Ile Arg Glu Val Ala Val							
	50		55		60		
Leu Arg His Leu Glu Thr Phe Glu His Pro Asn Val Val Arg Leu Phe							
	65		70		75		80
Asp Val Cys Thr Val Ser Arg Thr Asp Arg Glu Thr Lys Leu Thr Leu							
	85		90		95		
Val Phe Glu His Val Asp Gln Asp Leu Thr Thr Tyr Leu Asp Lys Val							
	100		105		110		
Pro Glu Pro Gly Val Pro Thr Glu Thr Ile Lys Asp Met Met Phe Gln							
	115		120		125		
Leu Leu Arg Gly Leu Asp Phe Leu His Ser His Arg Val Val His Arg							
	130		135		140		
Asp Leu Lys Pro Gln Asn Ile Leu Val Thr Ser Ser Gly Gln Ile Lys							
	145		150		155		160

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Leu Ala Asp Phe Gly Leu Ala Arg Ile Tyr Ser Phe Gln Met Ala Leu
 165 170 175
 Thr Ser Val Val Val Thr Leu Trp Tyr Arg Ala Pro Glu Val Leu Leu
 180 185 190
 Gln Ser Ser Tyr Ala Thr Pro Val Asp Leu Trp Ser Val Gly Cys Ile
 195 200 205
 Phe Ala Glu Met Phe Arg Arg Lys Pro Leu Phe Arg Gly Ser Ser Asp
 210 215 220
 Val Asp Gln Leu Gly Lys Ile Leu Asp Val Ile Gly Leu Pro Gly Glu
 225 230 235 240
 Glu Asp Trp Pro Arg Asp Val Ala Leu Pro Arg Gln Ala Phe His Ser
 245 250 255
 Lys Ser Ala Gln Pro Ile Glu Lys Phe Val Thr Asp Ile Asp Glu Leu
 260 265 270
 Gly Lys Asp Leu Leu Leu Lys Cys Leu Thr Phe Asn Pro Ala Lys Arg
 275 280 285
 Ile Ser Ala Tyr Ser Ala Leu Ser His Pro Tyr Phe Gln Asp Leu Glu
 290 295 300
 Arg Cys Lys Glu Asn Leu Asp Ser His Leu Pro Pro Ser Gln Asn Thr
 305 310 315 320
 Ser Glu Leu Asn Thr Ala
 325

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